



SEQUENCE LISTING

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JAN 06 2004

TECH CENTER 1600/2900

<110> Logemann, Juergen
Jach, Guido
Gornhardt, Birgit
Mundy, John
Schell, Jeff
Eckes, Peter
Chet, Ilan

<120> Transgenic pathogen-resistant organism

<130> A29542-FWC-I-R 070037.0195

<140> US 09/729,141

<141> 2000-12-01

<150> 08/812,025

<151> 1997-03-06

<150> 08/457,797

<151> 1995-06-01

<150> 08/134,416

<151> 1993-10-08

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 275

<212> DNA

<213> Aspergillus giganteus

<220>

<221> CDS

<222> (46)...(225)

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Met Gln Glu Met

1

aga gcg cgg gtt ttg gcc aca tac aat ggc aaa tgc tac aag aag gat 105
Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp

<210> 4
 <211> 1032
 <212> DNA
 <213> Hordeum vulgare

<220>
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 <222> (1)...(42)

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 <222> (43)...(885)

<221> 3'UTR
 <222> (886)...(1032)
 <223> 46 nucleotides at the 3' end not shown

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 <222> (930)...(935)
 <223> potential polyadenylation signal

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 <222> (1002)...(1011)
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<221> mat_peptide
 <222> (46)...(886)

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 Met Ala Lys Asn Val Asp Lys Pro Leu Phe Thr Ala Thr Phe Asn Val
 5 10 15 20

cag gcc agc tcc gcc gac tac gcc acc ttc atc gcc ggc atc cgc aac 150
 Gln Ala Ser Ser Ala Asp Tyr Ala Thr Phe Ile Ala Gly Ile Arg Asn
 25 30 35

aag ctc cgc aac ccg gcg cac ttc tcc cac aac cgc ccc gtg ctg ccg 198
 Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg Pro Val Leu Pro
 40 45 50

agg acg gct gta cag gcc gcc aac acg ctg ggg atc ctg ctg ttc gtg 822
 Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile Leu Leu Phe Val
 245 250 255 260

gag gtg ccg ggt ggg ttg acg gtg gcc aag gcg ctg gag ctg ttc cat 870
 Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
 265 270 275

gcg agt ggt ggg aaa taggtagttt tccaggtata cctgcatggg tagtgtaaaa 925
 Ala Ser Gly Gly Lys
 280

gtcgaataaa catgtcacag agtgacggac tgatataaat aaataaataa acgtgtcaca 985
 gagttacata taaacaaata aataaataat taaaaatgtc cagttta 1032

<210> 5

<211> 281

<212> PRT

<213> Hordeum vulgare

<400> 5

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		20					25						30		
Gly	Ile	Arg	Asn	Lys	Leu	Arg	Asn	Pro	Ala	His	Phe	Ser	His	Asn	Arg
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Pro	Val	Leu	Pro	Pro	Val	Glu	Pro	Asn	Val	Pro	Pro	Ser	Arg	Trp	Phe
	50					55					60				
His	Val	Val	Leu	Lys	Ala	Ser	Pro	Thr	Ser	Ala	Gly	Leu	Thr	Leu	Ala
65				70					75						80
Ile	Arg	Ala	Asp	Asn	Ile	Tyr	Leu	Glu	Gly	Phe	Lys	Ser	Ser	Asp	Gly
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Thr	Trp	Trp	Glu	Leu	Thr	Pro	Gly	Leu	Ile	Pro	Gly	[Gly]	Ala	Thr	Tyr	Val
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Thr	Asn	Val	Ala	Leu	Gly	Arg	Gln	Gln	Leu	[Pro]	Ala	Asp	Ala	Val	Thr	Ala
	130					135					140					

Leu	His	Gly	Arg	Thr	Lys	Ala	Asp	Lys	Pro	Ser	Gly	Pro	Lys	Gln	Gln
145					150				155					160	

Gln	Ala	Arg	Glu	Ala	Val	Thr	Thr	Leu	Leu	Leu	Met	Val	Asn	Glu	Ala
		165						170						175	

Thr	Arg	Phe	Gln	Thr	Val	Ser	Gly	Phe	Val	Ala	Gly	Leu	Leu	His	Pro
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Lys	Ala	Val	Glu	Lys	Lys	Ser	Gly	Lys	Ile	Gly	Asn	Glu	Met	Lys	Ala
	195					200					205				

Gln	Val	Asn	Gly	Trp	Gln	Asp	Leu	Ser	Ala	Ala	Leu	Leu	Lys	Thr	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ccg gtc gag ccc aac gtc ccg ccg agc agg tgg ttc cac gtc gtg ctc	246
Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe His Val Val Leu	
55 60 65	
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Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala Ile Arg Ala Asp	
70 75 80	
aac atc tac ctg gag ggc ttc aag agc agc gac ggc acc tgg tgg gag	342
Asn Ile Tyr Leu Glu Gly Phe Lys Ser Ser Asp Gly Thr Trp Trp Glu	
85 90 95 100	
ctc acc ccg ggc ctc atc ccc ggc gcc acc tac gtc ggg ttc ggc ggc	390
Leu Thr Pro Gly Leu Ile Pro Gly Ala Thr Tyr Val Gly Phe Gly Gly	
105 110 115	
acc tac cgc gac ctc ctc ggc gac acc gac aag ctg acc aac gtc gct	438
Thr Tyr Arg Asp Leu Leu Gly Asp Thr Asp Lys Leu Thr Asn Val Ala	
120 125 130	
CTC GGC CGG CAG CAG [CTC CCG] CTG GCG GAC GCG GTG ACC GCC CTC CAC GGG CGC	486
Leu Gly Arg Gln Gln [Leu Ala] Leu Ala Asp Ala Val Thr Ala Leu His Gly Arg	
135 140 145	
acc aag gcc gac aag ccg tcc ggc ccg aag cag cag cag gcg agg gag	534
Thr Lys Ala Asp Lys Pro Ser Gly Pro Lys Gln Gln Gln Ala Arg Glu	
150 155 160	
gcg gtg acg acg ctg ctc ctc atg gtg aac gag gcc acc cgg ttc cag	582
Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala Thr Arg Phe Gln	
165 170 175 180	
acg gtg tct ggg ttc gtg gcc ggg ttg ctg cac ccc aag gcg gtg gag	630
Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu	
185 190 195	
aag aag agc ggg aag atc ggc aat gag atg aag gcc cag gtg aac ggg	678
Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly	
200 205 210	
tgg cag gac ctg tcc gcg gcg ctg ctg aag acg gac gtg aag cct ccg	726
Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro	
215 220 225	
ccg gga aag tcg cca gcg aag ttc gcg ccg atc gag aag atg ggc gtg	774
Pro Gly Lys Ser Pro Ala Lys Phe Ala Pro Ile Glu Lys Met Gly Val	
230 235 240	

210		215		220											
Val	Lys	Pro	Pro	Pro	Gly	Lys	Ser	Pro	Ala	Lys	Phe	Ala	Pro	Ile	Glu
225					230					235					240
Lys	Met	Gly	Val	Arg	Thr	Ala	Val	Gln	Ala	Ala	Asn	Thr	Leu	Gly	Ile
				245					250					255	
Leu	Leu	Phe	Val	Glu	Val	Pro	Gly	Gly	Leu	Thr	Val	Ala	Lys	Ala	Leu
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Glu	Leu	Phe	His	Ala	Ser	Gly	Gly	Lys							
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 <212> DNA
 <213> Hordeum vulgare

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 <222> (404)...(409)
 <223> potential polyadenylation signal

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 acg gtg tcg ggg ttc gtg gcc ggg ctg ctg cac ccc aag gcg gtg gag 96
 Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu
 20 25 30

 aag aag agc ggg aag atc ggc aat gag atg aag gcc cag gtg aac ggg 144

Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly
 35 40 45

tgg cag gac ctg tcc gcg gcg ctg ctg aag acg gac gtg aag ccc ccg 192
 Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro
 50 55 60

ccg gga aag tcg cca gcg aag ttc acg ccg atc gag aag atg ggc gtg 240
 Pro Gly Lys Ser Pro Ala Lys Phe Thr Pro Ile Glu Lys Met Gly Val
 65 70 75 80

agg act gct gag cag gct gcg gct act ttg ggg atc ctg ctg ttc gtt 288
 Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val
 85 90 95

gag gtg ccg ggt ggg ttg acg gtg gcc aag gcg ctg gag ctg ttt cat 336
 Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
 100 105 110

gcg agt ggt ggg aaa taggtagttt tgcaggtata cctgcatggg taaatgtaaa 391
 Ala Ser Gly Gly Lys
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agtcgaataa aaatgtcaca gagtgacgga ctgatataaa taaattaata aacatgtcat 451
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<210> 7

<211> 117

<212> PRT

<213> Hordeum vulgare

<400> 7

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 35 40 45
 Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro
 50 55 60
 Pro Gly Lys Ser Pro Ala Lys Phe Thr Pro Ile Glu Lys Met Gly Val
 65 70 75 80
 Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val
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 Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
 100 105 110
 Ala Ser Gly Gly Lys
 115

<210> 8
<211> 2329
<212> DNA
<213> *Serratia marcescens*

<220>
<221> misc_feature
<222> (1)...(2329)
<223> ChiS gene from plasmid pLChis from E.coli A5187

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atgaaaataa attcacgctt gctgaataaa acccagttga tagcgctctt gtttttgcg 180
cttttttatt tatagtactg aatgtacgcg gtgggaatga ttatttcgcc acgtggaaag 240
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atgcgcaaat ttaataaacc gctggtggcg ctggtgatcg gcagcacgct gtgttccgcg 420
gcgcaggccg ccgcgccggg caagccgacc atcgccctggg gcaacaccaa gttcgccatc 480
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accgccagtg acgccaccga aattgtggtg gccgacaccg acggcagcca tttggcgccg 780
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atcgacgcgg ataacggcga tattctcaac agcatgaacg ccagcctggg caacagcgcc 2040
ggcgttcaat aatcggttgc agtggttgcc gggggatata ctttcgcccc cggttttttc 2100


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gccgacgaaa gttttttttac gccgcacaga ttgtggctct gccccgagca aaacgcgctc 2160
atcggactca cccttttggg taatccttca gcatttcctc ctgtctttaa cggcgatcac 2220
aaaaataacc gttcagatat tcatcattca gcaacaaagt ttggcggtt tttaacggag 2280
ttaaaaacca gtaagtttgt gagggtcaga ccaatgcgct aaaaatggg 2329

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<212> DNA

<213> Hordeum vulgare

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<222> (64)...(861)

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<222> (905)...(910)

<223> potential polyadenylation site

<221> sig_peptide

<222> (64)...(294)

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<221> sig_peptide

<222> (298)...(312)

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<221> sig_peptide

<222> (349)...(378)

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<222> (466)...(588)

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<222> (607)...(861)

<223> probable signal peptide

<221> mat_peptide

<222> (133)...(861)

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Met Arg Ser Leu Ala Val Val Val Ala Val Val Ala Thr Val Ala	
1 5 10 15	
atg gcc atc ggc acg gcg cgc ggc agc gtg tcc tcc atc gtc tcg cgc	156
Met Ala Ile Gly Thr Ala Arg Gly Ser Val Ser Ser Ile Val Ser Arg	
20 25 30	
gca cag ttt gac cgc atg ctt ctc cac cgc aac gac ggc gcc tgc cag	204
Ala Gln Phe Asp Arg Met Leu Leu His Arg Asn Asp Gly Ala Cys Gln	
35 40 45	
gcc aag ggc ttc tac acc tac gac gcc ttc gtc gcc gcc gca gcc gcc	252
Ala Lys Gly Phe Tyr Thr Tyr Asp Ala Phe Val Ala Ala Ala Ala Ala	
50 55 60	
ttc ccg ggc ttc ggc acc acc ggc agc gcc gac gcc cag aag cgc gag	300
Phe Pro Gly Phe Gly Thr Thr Gly Ser Ala Asp Ala Gln Lys Arg Glu	
65 70 75	
gtg gcc gcc ttc cta gca cag acc tcc cac gag acc acc ggc ggg tgg	348
Val Ala Ala Phe Leu Ala Gln Thr Ser His Glu Thr Thr Gly Gly Trp	
80 85 90 95	
gcg act gca ccg gac ggg gcc ttc gcc tgg ggc tac tgc ttc aag cag	396
Ala Thr Ala Pro Asp Gly Ala Phe Ala Trp Gly Tyr Cys Phe Lys Gln	
100 105 110	
gaa cgt ggc gcc tcc tcc gac tac tgc acc ccg agc gca caa tgg ccg	444
Glu Arg Gly Ala Ser Ser Asp Tyr Cys Thr Pro Ser Ala Gln Trp Pro	
115 120 125	
tgc gcc ccc ggg aag cgc tac tac ggc cgc ggg cca atc cag ctc tcc	492
Cys Ala Pro Gly Lys Arg Tyr Tyr Gly Arg Gly Pro Ile Gln Leu Ser	
130 135 140	
cac aac tac aac tat gga cct gcc ggc cgg gcc atc ggg gtc gat ctg	540
His Asn Tyr Asn Tyr Gly Pro Ala Gly Arg Ala Ile Gly Val Asp Leu	
145 150 155	
ctg gcc aac ccg gac ctg gtg gcc acg gac gcc act gtg ggc ttt aag	588
Leu Ala Asn Pro Asp Leu Val Ala Thr Asp Ala Thr Val Gly Phe Lys	
160 165 170 175	

acg gcc atc tgg ttc tgg atg acg gcg cag ccg ccc aag cca tcg agc	636
Thr Ala Ile Trp Phe Trp Met Thr Ala Gln Pro Pro Lys Pro Ser Ser	
180 185 190	

cat gct gtg atc gcc ggc cag tgg agc ccg tca ggg gct gac cgg gcc	684
His Ala Val Ile Ala Gly Gln Trp Ser Pro Ser Gly Ala Asp Arg Ala	
195 200 205	

gca ggc cgg gtg ccc ggg ttt ggt gtg atc acc aac atc atc aac ggc	732
Ala Gly Arg Val Pro Gly Phe Gly Val Ile Thr Asn Ile Ile Asn Gly	
210 215 220	

ggg atc gag tgc ggt cac ggg cag gac agc cgc gtc gcc gat cga atc	780
Gly Ile Glu Cys Gly His Gly Gln Asp Ser Arg Val Ala Asp Arg Ile	
225 230 235	

ggg ttt tac aag cgc tac tgt gac atc ctc ggc gtt ggc tac ggc aac	828
Gly Phe Tyr Lys Arg Tyr Cys Asp Ile Leu Gly Val Gly Tyr Gly Asn	
240 245 250 255	

aac ctc gat tgc tac agc cag aga ccc ttc gcc taattaatta gtcattgtatt	881
Asn Leu Asp Cys Tyr Ser Gln Arg Pro Phe Ala	
260 265	

aatcttggcc ctccataaaa tacaataaga gcatcgtctc ctatctacat gctgtaagat	941
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a	1002

<210> 10

<211> 266

<212> PRT

<213> Hordeum vulgare

<400> 10

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35 40 45	
Lys Gly Phe Tyr Thr Tyr Asp Ala Phe Val Ala Ala Ala Ala Ala Phe	
50 55 60	
Pro Gly Phe Gly Thr Thr Gly Ser Ala Asp Ala Gln Lys Arg Glu Val	
65 70 75 80	
Ala Ala Phe Leu Ala Gln Thr Ser His Glu Thr Thr Gly Gly Trp Ala	
85 90 95	

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Arg	Gly	Ala	Ser	Ser	Asp	Tyr	Cys	Thr	Pro	Ser	Ala	Gln	Trp	Pro	Cys
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Ala	Pro	Gly	Lys	Arg	Tyr	Tyr	Gly	Arg	Gly	Pro	Ile	Gln	Leu	Ser	His
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Asn	Tyr	Asn	Tyr	Gly	Pro	Ala	Gly	Arg	Ala	Ile	Gly	Val	Asp	Leu	Leu
145					150					155					160
Ala	Asn	Pro	Asp	Leu	Val	Ala	Thr	Asp	Ala	Thr	Val	Gly	Phe	Lys	Thr
			165					170						175	
Ala	Ile	Trp	Phe	Trp	Met	Thr	Ala	Gln	Pro	Pro	Lys	Pro	Ser	Ser	His
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Ala	Val	Ile	Ala	Gly	Gln	Trp	Ser	Pro	Ser	Gly	Ala	Asp	Arg	Ala	Ala
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Gly	Arg	Val	Pro	Gly	Phe	Gly	Val	Ile	Thr	Asn	Ile	Ile	Asn	Gly	Gly
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Ile	Glu	Cys	Gly	His	Gly	Gln	Asp	Ser	Arg	Val	Ala	Asp	Arg	Ile	Gly
225					230					235					240
Phe	Tyr	Lys	Arg	Tyr	Cys	Asp	Ile	Leu	Gly	Val	Gly	Tyr	Gly	Asn	Asn
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 <212> DNA
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<221> CDS
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<221> 3'UTR
 <222> (1051)...(1235)
 <223> partial, 14 nucleotides at the 3' end not shown

<221> polyA_signal
 <222> (1083)...(1088)
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<221> polyA_signal
 <222> (1210)...(1215)
 <223> potential polyadenylation signal

<221> mat_peptide
<222> (133)...(1050)

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					1	
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Lys Asp Val Ala Ser Met Phe Ala Val Ala Leu Phe Ile Gly Ala Phe						
5 10 15						
gct gct gtt cct acg agt gtg cag tcc atc ggc gta tgc tac ggc gtg	153					
Ala Ala Val Pro Thr Ser Val Gln Ser Ile Gly Val Cys Tyr Gly Val						
20 25 30 35						
atc ggc aac aac ctc ccc tcc cgg agc gac gtg gtg cag ctc tac agg	201					
Ile Gly Asn Asn Leu Pro Ser Arg Ser Asp Val Val Gln Leu Tyr Arg						
40 45 50						
tcc aag ggc atc aac ggc atg cgc atc tac ttc gcc gac ggg cag gcc	249					
Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp Gly Gln Ala						
55 60 65						
ctc tcg gcc gtc cgc aac tcc ggc atc ggc ctc atc ctc gac atc ggc	297					
Leu Ser Ala Val Arg Asn Ser Gly Ile Gly Leu Ile Leu Asp Ile Gly						
70 75 80						
aac gac cag ctc gcc aac atc gcc gcc agc acc tcc aac gcg gcc tcc	345					
Asn Asp Gln Leu Ala Asn Ile Ala Ala Ser Thr Ser Asn Ala Ala Ser						
85 90 95						
tgg gtc cag aac aac gtg cgg ccc tac tac cct gcc gtg aac atc aag	393					
Trp Val Gln Asn Asn Val Arg Pro Tyr Tyr Pro Ala Val Asn Ile Lys						
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Tyr Ile Ala Ala Gly Asn Glu Val Gln Gly Gly Ala Thr Gln Ser Ile						
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Leu Pro Ala Met Arg Asn Leu Asn Ala Ala Leu Ser Ala Ala Gly Leu						
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Gly Ala Ile Lys Val Ser Thr Ser Ile Arg Phe Asp Glu Val Ala Asn						
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Ser Phe Pro Pro Ser Ala Gly Val Phe Lys Asn Ala Tyr Met Thr Asp	
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Val Ala Arg Leu Leu Ala Ser Thr Gly Ala Pro Leu Leu Ala Asn Val	
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Tyr Ala Thr Phe Gln Pro Gly Thr Thr Val Arg Asp Gln Asn Asn Gly	
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Leu Thr Tyr Thr Ser Leu Phe Asp Ala Met Val Asp Ala Val Tyr Ala	
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Lys Lys Arg Glu Ala Leu Glu Thr Tyr Ile Phe Ala Met Phe Asn Glu	
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325

330